



## SEQUENCE LISTING

<110> FORSSMANN, WOLF-GEORG  
MAGERT, HANS-JURGEN  
STANDKER, LUDGER  
KREUZTMANN, PETER

<120> SERINE PROTEINASE INHIBITORS

<130> 10496/P65678US0

<140> 09/582,328  
<141> 2000-07-19

<150> PCT/EP98/08424  
<151> 1998-12-23

<150> DE 197 57 572.2  
<151> 1997-12-23

<160> 41

<170> PatentIn Ver. 2.1

<210> 1  
<211> 177  
<212> PRT  
<213> Unknown Organism

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<223> Description of Unknown Organism: VAKTI-1 amino acid sequence

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Met Lys Ile Ala Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu  
1 5 10 15

Ile Gln Asp Ala Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu  
20 25 30

Phe Gln Ala Phe Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys  
35 40 45

Lys Phe Phe Gln Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala  
50 55 60

Thr Cys Lys Met Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala  
65 70 75 80

Arg His Leu Ala Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn  
85 90 95

Cys Asp Asp Phe Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro  
100 105 110

Asp Tyr Tyr Glu Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn  
115 120 125

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Arg Cys Ala Leu Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly  
130 135 140

Val Lys Ser Glu Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Val Arg  
145 150 155 160

Ser Ile Val Ser Leu Met Gly Asn Thr Gly Arg Leu Thr Ser Asn Ser  
165 170 175

Lys

<210> 2

<211> 922

<212> PRT

<213> Unknown Organism

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<223> Description of Unknown Organism: VATKI-2 amino acid sequence

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Met Lys Ile Ala Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu  
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Ile Gln Asp Ala Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu  
20 25 30

Phe Gln Ala Phe Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys  
35 40 45

Lys Phe Phe Gln Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala  
50 55 60

Thr Cys Lys Met Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala  
65 70 75 80

Arg His Leu Ala Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn  
85 90 95

Cys Asp Asp Phe Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro  
100 105 110

Asp Tyr Tyr Glu Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn  
115 120 125

Arg Cys Ala Leu Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly  
130 135 140

Val Lys Ser Glu Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Asp Val  
145 150 155 160

Cys Ser Ala Phe Arg Pro Phe Val Arg Asn Gly Arg Leu Gly Cys Thr  
165 170 175

Arg Glu Asn Asp Pro Val Leu Gly Pro Asp Gly Lys Thr His Gly Asn  
180 185 190

Lys Cys Ala Met Cys Ala Glu Leu Phe Leu Lys Glu Ala Glu Asn Ala  
 195 200 205

Lys Arg Glu Gly Glu Thr Arg Ile Arg Arg Asn Ala Glu Lys Asp Phe  
 210 215 220

Cys Lys Glu Tyr Glu Lys Gln Val Arg Asn Gly Arg Leu Phe Cys Thr  
 225 230 235 240

Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly Arg Met His Gly Asn  
 245 250 255

Lys Cys Ala Leu Cys Ala Glu Ile Phe Lys Arg Arg Phe Ser Glu Glu  
 260 265 270

Asn Ser Lys Thr Asp Gln Asn Leu Gly Lys Ala Glu Glu Lys Thr Lys  
 275 280 285

Val Lys Arg Glu Ile Val Lys Leu Cys Ser Gln Tyr Gln Asn Gln Ala  
 290 295 300

Lys Asn Gly Ile Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Arg Gly  
 305 310 315 320

Pro Asp Gly Lys Met His Gly Asn Leu Cys Ser Met Cys Gln Val Tyr  
 325 330 335

B  
 Phe Gln Ala Glu Asn Glu Glu Lys Lys Lys Ala Glu Ala Arg Ala Arg  
 340 345 350

Asn Lys Arg Glu Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn  
 355 360 365

Glu Tyr Arg Lys Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu  
 370 375 380

Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys  
 385 390 395 400

Ser Met Cys Glu Val Phe Phe Gln Ala Glu Glu Glu Lys Lys Lys  
 405 410 415

Lys Glu Gly Glu Ser Arg Asn Lys Arg Gln Ser Lys Ser Thr Ala Ser  
 420 425 430

Phe Glu Glu Leu Cys Ser Glu Tyr Arg Lys Ser Arg Lys Asn Gly Arg  
 435 440 445

Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys  
 450 455 460

Met His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln Gln Glu  
 465 470 475 480

Glu Arg Ala Arg Ala Lys Ala Lys Arg Glu Ala Ala Lys Glu Ile Cys  
 485 490 495

Ser Glu Phe Arg Asp Gln Val Arg Asn Gly Thr Leu Ile Cys Thr Arg  
500 505 510

Glu His Asn Pro Val Arg Gly Pro Asp Gly Lys Met His Gly Asn Lys  
515 520 525

Cys Ala Met Cys Ala Ser Val Phe Lys Leu Glu Glu Glu Lys Lys  
530 535 540

Asn Asp Lys Glu Glu Lys Gly Lys Val Glu Ala Glu Lys Val Lys Arg  
545 550 555 560

Glu Ala Val Gln Glu Leu Cys Ser Glu Tyr Arg His Tyr Val Arg Asn  
565 570 575

Gly Arg Leu Pro Cys Thr Arg Glu Asn Asp Pro Ile Glu Gly Leu Asp  
580 585 590

Gly Lys Ile His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln  
595 600 605

Gln Glu Ala Lys Glu Lys Glu Arg Ala Glu Pro Arg Ala Lys Val Lys  
610 615 620

Arg Glu Ala Glu Lys Glu Thr Cys Asp Glu Phe Arg Arg Leu Leu Gln  
625 630 635 640

Asn Gly Lys Leu Phe Cys Thr Arg Glu Asn Asp Pro Val Arg Gly Pro  
645 650 655

Asp Gly Lys Thr His Gly Asn Lys Cys Ala Met Cys Lys Ala Val Phe  
660 665 670

Gln Lys Glu Asn Glu Glu Arg Lys Arg Lys Glu Glu Asp Gln Arg  
675 680 685

Asn Ala Ala Gly His Gly Ser Ser Gly Gly Gly Asn Thr Gln  
690 695 700

Asp Glu Cys Ala Glu Tyr Arg Glu Gln Met Lys Asn Gly Arg Leu Ser  
705 710 715 720

Cys Thr Arg Glu Ser Asp Pro Val Arg Asp Ala Asp Gly Lys Ser Tyr  
725 730 735

Asn Asn Gln Cys Thr Met Cys Lys Ala Lys Leu Glu Arg Glu Ala Glu  
740 745 750

Arg Lys Asn Glu Tyr Ser Arg Ser Arg Ser Asn Gly Thr Gly Ser Glu  
755 760 765

Ser Gly Lys Asp Thr Cys Asp Glu Phe Arg Ser Gln Met Lys Asn Gly  
770 775 780

Lys Leu Ile Cys Thr Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly  
785 790 795 800

Lys Thr His Gly Asn Lys Cys Thr Met Cys Lys Glu Lys Leu Glu Arg  
 805 810 815  
 Glu Ala Ala Glu Lys Lys Arg Lys Arg Met Lys Thr Gly Ala Ile Gln  
 820 825 830  
 Glu Lys Gly Ala Ile Gln Glu Lys Gly Ala Met Thr Lys Arg Ile Cys  
 835 840 845  
 Val Val Asn Phe Glu Ala Cys Arg Glu Met Glu Ser Leu Ser Ala Pro  
 850 855 860  
 Glu Lys Ile Thr Leu Phe Glu Ala His Met Ala Arg Cys Thr Ser Ile  
 865 870 875 880  
 Asn Val Leu Cys Val Arg Ala Ser Leu Ile Glu Lys Leu Met Lys Glu  
 885 890 895  
 Lys Arg Lys Met Lys Arg Asn Gln Val Ala Ser Pro Gln Ile Met Gln  
 900 905 910  
 Arg Met Ser Ala Val Asn Phe Glu Thr Ile  
 915 920

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 <213> Unknown Organism  
  
 <220>  
 <223> Description of Unknown Organism: HF 6479 amino  
 acid sequence

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 Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys Lys Phe Phe Gln Ser Leu  
 20 25 30  
 Asp Gly Ile Met Phe Ile Asn Lys Cys Ala Thr Cys Lys Met Ile Leu  
 35 40 45  
 Glu Lys Glu Ala Lys Ser Gln  
 50 55

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 <212> PRT  
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 <223> Description of Unknown Organism: HF 7665 amino  
 acid sequence

<400> 4  
 Glu Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn Glu Tyr Arg  
 1 5 10 15

Lys Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu Asn Asp Pro  
 20 25 30

Ile Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys Ser Met Cys  
 35 40 45

Glu Val Phe Phe Gln Ala Glu Glu Glu Lys Lys Lys Lys Glu Gly  
 50 55 60

Glu Ser Arg Asn  
 65

<210> 5

<211> 748

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: VAKTI-1 cDNA  
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<221> CDS

<222> (43) .. (573)

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 Met Lys Ile Ala  
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aca gtg tca gtg ctt ctg ccc ttg gct ctt tgc ctc ata caa gat gct 102  
 Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu Ile Gln Asp Ala  
 5 10 15 20

gcc agt aag aat gaa gat cag gaa atg tgc cat gaa ttt cag gca ttt 150  
 Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu Phe Gln Ala Phe  
 25 30 35

atg aaa aat gga aaa ctg ttc tgt ccc cag gat aag aaa ttt ttt caa 198  
 Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys Phe Phe Gln  
 40 45 50

agt ctt gat gga ata atg ttc atc aat aaa tgt gcc acg tgc aaa atg 246  
 Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala Thr Cys Lys Met  
 55 60 65

ata ctg gaa aaa gaa gca aaa tca cag aag agg gcc agg cat tta gca 294  
 Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala Arg His Leu Ala  
 70 75 80

aga gct ccc aag gct act gcc cca aca gag ctg aat tgt gat gat ttt 342  
 Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn Cys Asp Asp Phe  
 85 90 95 100

aaa aaa gga gaa aga gat ggg gat ttt atc tgt cct gat tat tat gaa	390
Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro Asp Tyr Tyr Glu	
105 110 115	
gct gtt tgt ggc aca gat ggg aaa aca tat gac aac aga tgt gca ctg	438
Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn Arg Cys Ala Leu	
120 125 130	
tgt gct gag aat gcg aaa acc ggg tcc caa att ggt gta aaa agt gaa	486
Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly Val Lys Ser Glu	
135 140 145	
ggg gaa tgt aag agc agt aat cca gag cag gtg agg tca att gtc agc	534
Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Val Arg Ser Ile Val Ser	
150 155 160	
ctg atg gga aat act ggg agg cta act tca aat agt aag taggtgctgt	583
Leu Met Gly Asn Thr Gly Arg Leu Thr Ser Asn Ser Lys	
165 170 175	
cctcttcctt ctttaggtggg agccttgaa ggaattaatt cttgctttat gtgaaatgga	643
atacccaagg actgcccact aatatgaaaa agctaattat agtctctgaa actggatcag	703
attactttgg tggtaagat cttcaatct attgctgctt tgtat	748

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Met Lys Ile Ala	
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aca gtg tca gtg ctt ctg ccc ttg gct ctt tgc ctc ata caa gat gct	102
Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu Ile Gln Asp Ala	
5 10 15 20	
gcc agt aag aat gaa gat cag gaa atg tgc cat gaa ttt cag gca ttt	150
Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu Phe Gln Ala Phe	
25 30 35	
atg aaa aat gga aaa ctg ttc tgt ccc cag gat aag aaa ttt ttt caa	198
Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys Lys Phe Phe Gln	
40 45 50	

agt ctt gat gga ata atg ttc atc aat aaa tgt gcc acg tgc aaa atg 246  
 Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala Thr Cys Lys Met  
       55                 60                 65

ata ctg gaa aaa gaa gca aaa tca cag aag agg gcc agg cat tta gca 294  
 Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala Arg His Leu Ala  
       70                 75                 80

aga gct ccc aag gct act gcc cca aca gag ctg aat tgt gat gat ttt 342  
 Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn Cys Asp Asp Phe  
       85                 90                 95                 100

aaa aaa gga gaa aga gat ggg gat ttt atc tgt cct gat tat tat gaa 390  
 Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro Asp Tyr Tyr Glu  
       105                 110                 115

gct gtt tgt ggc aca gat ggg aaa aca tat gac aac aga tgt gca ctg 438  
 Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn Arg Cys Ala Leu  
       120                 125                 130

tgt gct gag aat gcg aaa acc ggg tcc caa att ggt gta aaa agt gaa 486  
 Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly Val Lys Ser Glu  
       135                 140                 145

ggg gaa tgt aag agc agt aat cca gag cag gat gta tgc agt gct ttt 534  
 Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Asp Val Cys Ser Ala Phe  
       150                 155                 160

,1  
 6  
 cont.

cg<sup>g</sup> ccc ttt gtt aga aat gga aga ctt gga tgc aca agg gaa aat gat 582  
 Arg Pro Phe Val Arg Asn Gly Arg Leu Gly Cys Thr Arg Glu Asn Asp  
       165                 170                 175                 180

cct gtt ctt ggt cct gat ggg aag acg cat ggc aat aag tgt gca atg 630  
 Pro Val Leu Gly Pro Asp Gly Lys Thr His Gly Asn Lys Cys Ala Met  
       185                 190                 195

tgt gct gag ctg ttt tta aaa gaa gct gaa aat gcc aag cga gag ggt 678  
 Cys Ala Glu Leu Phe Leu Lys Glu Ala Glu Asn Ala Lys Arg Glu Gly  
       200                 205                 210

gaa act aga att cga cga aat gct gaa aag gat ttt tgc aag gaa tat 726  
 Glu Thr Arg Ile Arg Arg Asn Ala Glu Lys Asp Phe Cys Lys Glu Tyr  
       215                 220                 225

gaa aaa caa gtg aga aat gga agg ctt ttt tgt aca cgg gag agt gat 774  
 Glu Lys Gln Val Arg Asn Gly Arg Leu Phe Cys Thr Arg Glu Ser Asp  
       230                 235                 240

cca gtc cgt ggc cct gac ggc agg atg cat ggc aac aaa tgt gcc ctg 822  
 Pro Val Arg Gly Pro Asp Gly Arg Met His Gly Asn Lys Cys Ala Leu  
       245                 250                 255                 260

tgt gct gaa att ttc aag cgg cgt ttt tca gag gaa aac agt aaa aca 870  
 Cys Ala Glu Ile Phe Lys Arg Arg Phe Ser Glu Glu Asn Ser Lys Thr  
       265                 270                 275

gat caa aat ttg gga aaa gct gaa gaa aaa act aaa gtt aaa aga gaa	918																																																																																																										
Asp Gln Asn Leu Gly Lys Ala Glu Glu Lys Thr Lys Val Lys Arg Glu																																																																																																											
280	285	290		att gtg aaa ctc tgc agt caa tat caa aat cag gca aag aat gga ata	966	Ile Val Lys Leu Cys Ser Gln Tyr Gln Asn Gln Ala Lys Asn Gly Ile		295	300	305		ctt ttc tgt acc aga gaa aat gac cct att cgt ggt cca gat ggg aaa	1014	Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Arg Gly Pro Asp Gly Lys		310	315	320		atg cat ggc aac ttg tgt tcc atg tgt caa gtc tac ttc caa gca gaa	1062	Met His Gly Asn Leu Cys Ser Met Cys Gln Val Tyr Phe Gln Ala Glu		325	330	340		aat gaa gaa aag aaa aag gct gaa gca cga gct aga aac aaa aga gaa	1110	Asn Glu Glu Lys Lys Ala Glu Ala Arg Ala Arg Asn Lys Arg Glu		345	350	355		tct gga aaa gca acc tca tat gca gag ctt tgc aat gaa tat cga aag	1158	Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn Glu Tyr Arg Lys		360	365	370		ctt gtg agg aac gga aaa ctt gct tgc acc aga gag aac gat cct att	1205	Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu Asn Asp Pro Ile		375	380	385		cag ggc cca gat ggg aaa gtg cac ggc aac acc tgc tcc atg tgt gag	1254	Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys Ser Met Cys Glu		390	395	400		gtt ttt ttc caa gca gaa gaa aag aaa aag aag gaa ggc gaa	1302	Val Phe Phe Gln Ala Glu Glu Glu Lys Lys Lys Glu Gly Glu		405	410	415	420	tca aga aac aaa aga caa tct aag agt aca gct tcc ttt gag gag ttg	1350	Ser Arg Asn Lys Arg Gln Ser Lys Ser Thr Ala Ser Phe Glu Glu Leu		425	430	435		tgt agt gaa tac cgc aaa tcc agg aaa aac gga cgg ctt ttt tgc acc	1398	Cys Ser Glu Tyr Arg Lys Ser Arg Lys Asn Gly Arg Leu Phe Cys Thr		440	445	450		aga gag aat gac ccc atc cag ggc cca gat ggg aaa atg cat ggc aac	1446	Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Met His Gly Asn		455	460	465		acc tgc tcc atg tgt gag gcc ttc ttt caa caa gaa gaa aga gca aga	1494	Thr Cys Ser Met Cys Glu Ala Phe Phe Gln Gln Glu Glu Arg Ala Arg		470	475	480		gca aag gct aaa aga gaa gct gca aag gaa atc tgc agt gaa ttt cgg	1542	Ala Lys Ala Lys Arg Glu Ala Ala Lys Glu Ile Cys Ser Glu Phe Arg		485	490	495	500
290																																																																																																											
att gtg aaa ctc tgc agt caa tat caa aat cag gca aag aat gga ata	966																																																																																																										
Ile Val Lys Leu Cys Ser Gln Tyr Gln Asn Gln Ala Lys Asn Gly Ile																																																																																																											
295	300	305		ctt ttc tgt acc aga gaa aat gac cct att cgt ggt cca gat ggg aaa	1014	Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Arg Gly Pro Asp Gly Lys		310	315	320		atg cat ggc aac ttg tgt tcc atg tgt caa gtc tac ttc caa gca gaa	1062	Met His Gly Asn Leu Cys Ser Met Cys Gln Val Tyr Phe Gln Ala Glu		325	330	340		aat gaa gaa aag aaa aag gct gaa gca cga gct aga aac aaa aga gaa	1110	Asn Glu Glu Lys Lys Ala Glu Ala Arg Ala Arg Asn Lys Arg Glu		345	350	355		tct gga aaa gca acc tca tat gca gag ctt tgc aat gaa tat cga aag	1158	Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn Glu Tyr Arg Lys		360	365	370		ctt gtg agg aac gga aaa ctt gct tgc acc aga gag aac gat cct att	1205	Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu Asn Asp Pro Ile		375	380	385		cag ggc cca gat ggg aaa gtg cac ggc aac acc tgc tcc atg tgt gag	1254	Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys Ser Met Cys Glu		390	395	400		gtt ttt ttc caa gca gaa gaa aag aaa aag aag gaa ggc gaa	1302	Val Phe Phe Gln Ala Glu Glu Glu Lys Lys Lys Glu Gly Glu		405	410	415	420	tca aga aac aaa aga caa tct aag agt aca gct tcc ttt gag gag ttg	1350	Ser Arg Asn Lys Arg Gln Ser Lys Ser Thr Ala Ser Phe Glu Glu Leu		425	430	435		tgt agt gaa tac cgc aaa tcc agg aaa aac gga cgg ctt ttt tgc acc	1398	Cys Ser Glu Tyr Arg Lys Ser Arg Lys Asn Gly Arg Leu Phe Cys Thr		440	445	450		aga gag aat gac ccc atc cag ggc cca gat ggg aaa atg cat ggc aac	1446	Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Met His Gly Asn		455	460	465		acc tgc tcc atg tgt gag gcc ttc ttt caa caa gaa gaa aga gca aga	1494	Thr Cys Ser Met Cys Glu Ala Phe Phe Gln Gln Glu Glu Arg Ala Arg		470	475	480		gca aag gct aaa aga gaa gct gca aag gaa atc tgc agt gaa ttt cgg	1542	Ala Lys Ala Lys Arg Glu Ala Ala Lys Glu Ile Cys Ser Glu Phe Arg		485	490	495	500								
305																																																																																																											
ctt ttc tgt acc aga gaa aat gac cct att cgt ggt cca gat ggg aaa	1014																																																																																																										
Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Arg Gly Pro Asp Gly Lys																																																																																																											
310	315	320		atg cat ggc aac ttg tgt tcc atg tgt caa gtc tac ttc caa gca gaa	1062	Met His Gly Asn Leu Cys Ser Met Cys Gln Val Tyr Phe Gln Ala Glu		325	330	340		aat gaa gaa aag aaa aag gct gaa gca cga gct aga aac aaa aga gaa	1110	Asn Glu Glu Lys Lys Ala Glu Ala Arg Ala Arg Asn Lys Arg Glu		345	350	355		tct gga aaa gca acc tca tat gca gag ctt tgc aat gaa tat cga aag	1158	Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn Glu Tyr Arg Lys		360	365	370		ctt gtg agg aac gga aaa ctt gct tgc acc aga gag aac gat cct att	1205	Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu Asn Asp Pro Ile		375	380	385		cag ggc cca gat ggg aaa gtg cac ggc aac acc tgc tcc atg tgt gag	1254	Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys Ser Met Cys Glu		390	395	400		gtt ttt ttc caa gca gaa gaa aag aaa aag aag gaa ggc gaa	1302	Val Phe Phe Gln Ala Glu Glu Glu Lys Lys Lys Glu Gly Glu		405	410	415	420	tca aga aac aaa aga caa tct aag agt aca gct tcc ttt gag gag ttg	1350	Ser Arg Asn Lys Arg Gln Ser Lys Ser Thr Ala Ser Phe Glu Glu Leu		425	430	435		tgt agt gaa tac cgc aaa tcc agg aaa aac gga cgg ctt ttt tgc acc	1398	Cys Ser Glu Tyr Arg Lys Ser Arg Lys Asn Gly Arg Leu Phe Cys Thr		440	445	450		aga gag aat gac ccc atc cag ggc cca gat ggg aaa atg cat ggc aac	1446	Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Met His Gly Asn		455	460	465		acc tgc tcc atg tgt gag gcc ttc ttt caa caa gaa gaa aga gca aga	1494	Thr Cys Ser Met Cys Glu Ala Phe Phe Gln Gln Glu Glu Arg Ala Arg		470	475	480		gca aag gct aaa aga gaa gct gca aag gaa atc tgc agt gaa ttt cgg	1542	Ala Lys Ala Lys Arg Glu Ala Ala Lys Glu Ile Cys Ser Glu Phe Arg		485	490	495	500																
320																																																																																																											
atg cat ggc aac ttg tgt tcc atg tgt caa gtc tac ttc caa gca gaa	1062																																																																																																										
Met His Gly Asn Leu Cys Ser Met Cys Gln Val Tyr Phe Gln Ala Glu																																																																																																											
325	330	340		aat gaa gaa aag aaa aag gct gaa gca cga gct aga aac aaa aga gaa	1110	Asn Glu Glu Lys Lys Ala Glu Ala Arg Ala Arg Asn Lys Arg Glu		345	350	355		tct gga aaa gca acc tca tat gca gag ctt tgc aat gaa tat cga aag	1158	Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn Glu Tyr Arg Lys		360	365	370		ctt gtg agg aac gga aaa ctt gct tgc acc aga gag aac gat cct att	1205	Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu Asn Asp Pro Ile		375	380	385		cag ggc cca gat ggg aaa gtg cac ggc aac acc tgc tcc atg tgt gag	1254	Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys Ser Met Cys Glu		390	395	400		gtt ttt ttc caa gca gaa gaa aag aaa aag aag gaa ggc gaa	1302	Val Phe Phe Gln Ala Glu Glu Glu Lys Lys Lys Glu Gly Glu		405	410	415	420	tca aga aac aaa aga caa tct aag agt aca gct tcc ttt gag gag ttg	1350	Ser Arg Asn Lys Arg Gln Ser Lys Ser Thr Ala Ser Phe Glu Glu Leu		425	430	435		tgt agt gaa tac cgc aaa tcc agg aaa aac gga cgg ctt ttt tgc acc	1398	Cys Ser Glu Tyr Arg Lys Ser Arg Lys Asn Gly Arg Leu Phe Cys Thr		440	445	450		aga gag aat gac ccc atc cag ggc cca gat ggg aaa atg cat ggc aac	1446	Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Met His Gly Asn		455	460	465		acc tgc tcc atg tgt gag gcc ttc ttt caa caa gaa gaa aga gca aga	1494	Thr Cys Ser Met Cys Glu Ala Phe Phe Gln Gln Glu Glu Arg Ala Arg		470	475	480		gca aag gct aaa aga gaa gct gca aag gaa atc tgc agt gaa ttt cgg	1542	Ala Lys Ala Lys Arg Glu Ala Ala Lys Glu Ile Cys Ser Glu Phe Arg		485	490	495	500																								
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aat gaa gaa aag aaa aag gct gaa gca cga gct aga aac aaa aga gaa	1110																																																																																																										
Asn Glu Glu Lys Lys Ala Glu Ala Arg Ala Arg Asn Lys Arg Glu																																																																																																											
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Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys Ser Met Cys Glu																																																																																																											
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400																																																																																																											
gtt ttt ttc caa gca gaa gaa aag aaa aag aag gaa ggc gaa	1302																																																																																																										
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gtc cgt gga cca gat ggc aaa atg cat gga aac aag tgt gcc atg tgt		1638	
Val Arg Gly Pro Asp Gly Lys Met His Gly Asn Lys Cys Ala Met Cys			
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gcc agt gtg ttc aaa ctt gaa gaa gag aag aaa aat gat aaa gaa		1685	
Ala Ser Val Phe Lys Leu Glu Glu Glu Lys Lys Asn Asp Lys Glu			
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gaa aaa ggg aaa gtt gag gct gaa aaa gtt aag aga gaa gca gtt cag		1734	
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Cys Thr Arg Glu Asn Asp Pro Ile Glu Gly Leu Asp Gly Lys Ile His			
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<220>  
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&lt;220&gt;

&lt;223&gt; Description of Unknown Organism: Serine protease inhibitor

&lt;400&gt; 21

Thr Arg Glu Asn Asp Pro Val Leu Gly Pro Asp Gly Lys Thr His Gly  
1 5 10 15

Asn Lys

&lt;210&gt; 22

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Unknown Organism

&lt;220&gt;

&lt;223&gt; Description of Unknown Organism: Serine protease inhibitor

&lt;400&gt; 22

Thr Arg Glu His Asn Pro Val Arg Gly Pro Asp Gly Lys Met His Gly  
1 5 10 15

Asn Lys

*b*  
*cont.*  
<210> 23

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Unknown Organism

&lt;220&gt;

&lt;223&gt; Description of Unknown Organism: Serine protease inhibitor

&lt;400&gt; 23

Thr Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly Arg Met His Gly  
1 5 10 15

Asn Lys

&lt;210&gt; 24

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Unknown Organism

&lt;220&gt;

&lt;223&gt; Description of Unknown Organism: Serine protease inhibitor

<400> 24  
Thr Arg Glu Asn Asp Pro Ile Glu Gly Leu Asp Gly Lys Ile His Gly  
1 5 10 15

Asn Thr

<210> 25  
<211> 18  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Serine protease  
inhibitor

<400> 25  
Thr Arg Glu Asn Asp Pro Ile Arg Gly Pro Asp Gly Lys Met His Gly  
1 5 10 15

Asn Leu

<210> 26  
<211> 18  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Serine protease  
inhibitor

<400> 26  
Thr Arg Glu Asn Asp Pro Val Arg Gly Pro Asp Gly Lys Thr His Gly  
1 5 10 15

Asn Lys

<210> 27  
<211> 18  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Serine protease  
inhibitor

<400> 27  
Thr Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Val His Gly  
1 5 10 15

Asn Thr

<210> 28  
<211> 18  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Serine protease inhibitor

<400> 28  
Thr Arg Glu Ser Asp Pro Val Arg Asp Ala Asp Gly Lys Ser Tyr Asn  
1 5 10 15

Asn Gln

<210> 29  
<211> 18  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Serine protease inhibitor

<400> 29  
Thr Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly Lys Thr His Gly  
1 5 10 15

Asn Lys

<210> 30  
<211> 37  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Serine protease inhibitor

<400> 30  
Cys His Glu Phe Gln Ala Phe Met Lys Asn Gly Lys Leu Phe Cys Pro  
1 5 10 15

Gln Asp Lys Lys Phe Phe Gln Ser Leu Asp Gly Ile Met Phe Ile Asn  
20 25 30

Lys Cys Ala Thr Cys  
35

<210> 31  
<211> 37

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease inhibitor

<400> 31

Cys Asp Asp Phe Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro  
1 5 10 15

Asp Tyr Tyr Glu Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn  
20 25 30

Arg Cys Ala Leu Cys

35

<210> 32

<211> 37

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease inhibitor

<400> 32

Cys Ser Ala Phe Arg Pro Phe Val Arg Asn Gly Arg Leu Gly Cys Thr  
1 5 10 15

Arg Glu Asn Asp Pro Val Leu Gly Pro Asp Gly Lys Thr His Gly Asn  
20 25 30

Lys Cys Ala Met Cys

35

<210> 33

<211> 37

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease inhibitor

<400> 33

Cys Lys Glu Tyr Glu Lys Gln Val Arg Asn Gly Arg Leu Phe Cys Thr  
1 5 10 15

Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly Arg Met His Gly Asn  
20 25 30

Lys Cys Ala Leu Cys

35

<210> 34  
<211> 37  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Serine protease inhibitor

<400> 34  
Cys Ser Gln Tyr Gln Asn Gln Ala Lys Asn Gly Ile Leu Phe Cys Thr  
1 5 10 15  
Arg Glu Asn Asp Pro Ile Arg Gly Pro Asp Gly Lys Met His Gly Asn  
20 25 30  
Leu Cys Ser Met Cys  
35

<210> 35  
<211> 37  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Serine protease inhibitor

<400> 35  
Cys Asn Glu Tyr Arg Lys Leu Val Arg Asn Gly Lys Leu Ala Cys Thr  
1 5 10 15  
Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Val His Gly Asn  
20 25 30  
Thr Cys Ser Met Cys  
35

<210> 36  
<211> 37  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Serine protease inhibitor

<400> 36  
Cys Ser Glu Tyr Arg Lys Ser Arg Lys Asn Gly Arg Leu Phe Cys Thr  
1 5 10 15  
Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Met His Gly Asn  
20 25 30

Thr Cys Ser Met Cys  
35

<210> 37  
<211> 37  
<212> PRT  
<213> Unknown Organism  
  
<220>  
<223> Description of Unknown Organism: Serine protease inhibitor  
  
<400> 37

Cys Ser Glu Phe Arg Asp Gln Val Arg Asn Gly Thr Leu Ile Cys Thr  
1 5 10 15

Arg Glu His Asn Pro Val Arg Gly Pro Asp Gly Lys Met His Gly Asn  
20 25 30

Lys Cys Ala Met Cys  
35

<210> 38  
<211> 37  
<212> PRT  
<213> Unknown Organism  
  
<220>  
<223> Description of Unknown Organism: Serine protease inhibitor  
  
<400> 38

Cys Ser Glu Tyr Arg His Tyr Val Arg Asn Gly Arg Leu Pro Cys Thr  
1 5 10 15

Arg Glu Asn Asp Pro Ile Glu Gly Leu Asp Gly Lys Ile His Gly Asn  
20 25 30

Thr Cys Ser Met Cys  
35

<210> 39  
<211> 37  
<212> PRT  
<213> Unknown Organism  
  
<220>  
<223> Description of Unknown Organism: Serine protease inhibitor  
  
<400> 39

Cys Asp Glu Phe Arg Arg Leu Leu Gln Asn Gly Lys Leu Phe Cys Thr  
1 5 10 15

Arg Glu Asn Asp Pro Val Arg Gly Pro Asp Gly Lys Thr His Gly Asn  
20 25 30

Lys Cys Ala Met Cys  
35

<210> 40  
<211> 37  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Serine protease  
inhibitor

<400> 40  
Cys Ala Glu Tyr Arg Glu Gln Met Lys Asn Gly Arg Leu Ser Cys Thr  
1 5 10 15

Arg Glu Ser Asp Pro Val Arg Asp Ala Asp Gly Lys Ser Tyr Asn Asn  
20 25 30

Gln Cys Thr Met Cys  
35

<210> 41  
<211> 37  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Serine protease  
inhibitor

<400> 41  
Cys Asp Glu Phe Arg Ser Gln Met Lys Asn Gly Lys Leu Ile Cys Thr  
1 5 10 15

Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly Lys Thr His Gly Asn  
20 25 30

Lys Cys Thr Met Cys  
35